WHAT IS CLAIMED IS:

1. A composition for detecting an HIV-2 nucleic acid sequence, comprising:

a first amplification oligonucleotide comprising a sequence of 9-34 contiguous bases contained within the sequence of SEQ ID NO:9, said first amplification oligonucleotide having a length of up to 100 nucleotides; and

a second amplification oligonucleotide comprising a sequence of 19-40 contiguous bases from the sequence of SEQ ID NO:1, said second amplification oligonucleotide having a length of up to 100 nucleotides.

2. The composition of Claim 1, wherein the length of the second amplification oligonucleotide is 19-40 nucleotides.

3. The composition of Claim 2, wherein the length of the first amplification oligonucleotide is 18-60 nucleotides.

4. The composition of Claim 3, wherein the length of the first amplification oligonucleotide is 18-34 nucleotides.

5. The composition of Claim 4, wherein the length of the first amplification oligonucleotide is 18-25 nucleotides.

6. The composition of Claim 5, wherein the sequence of the first amplification oligonucleotide is selected from the group consisting of SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13 and SEQ ID NO:14.

7. The composition of Claim 2, wherein the length of the first amplification oligonucleotide is 18-60 nucleotides, and wherein the first amplification oligonucleotide further comprises a promoter sequence.

8. The composition of Claim 2, wherein the length of the second amplification oligonucleotide is 19-21 nucleotides.

9. The composition of Claim 8, wherein the length of the first amplification oligonucleotide is 18-34 nucleotides.

10. The composition of Claim 3, wherein the length of the second amplification oligonucleotide is 19-21 nucleotides.

11. The composition of Claim 7, wherein the first amplification oligonucleotide is a promoter-primer selected from the group consisting of SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18 and SEQ ID NO:19.

12. The composition of Claim 10, wherein the second amplification oligonucleotide

is selected from the group consisting of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 and SEQ ID NO:7.

13. The composition of Claim 10, wherein the first amplification oligonucleotide further comprises a promoter sequence.

14. The composition of Claim 13, wherein the first amplification oligonucleotide is a promoter-primer selected from the group consisting of SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18 and SEQ ID NO:19.

15. The composition of Claim 13, wherein the second amplification oligonucleotide is selected from the group consisting of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 and SEQ ID NO:7.

16. The composition of Claim 14, wherein the second amplification oligonucleotide is selected from the group consisting of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 and SEQ ID NO:7.

17. The composition of Claim 1, wherein the length of the first amplification oligonucleotide is 18-25 nucleotides, and wherein the length of the second amplification oligonucleotide is 19-21 nucleotides.

18. The composition of Claim 17, wherein the first amplification oligonucleotide is selected from the group consisting of SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13 and SEQ ID NO:14.

19. The composition of Claim 17, wherein the second amplification oligonucleotide is selected from the group consisting of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 and SEQ ID NO:7.

20. The composition of Claim 18, wherein the second amplification oligonucleotide is selected from the group consisting of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 and SEQ ID NO:7.

21. The composition of Claim 1, further comprising an oligonucleotide detection probe having a sequence that comprises SEQ ID NO:21 or the complement thereof.

22. The composition of Claim 21, wherein said oligonucleotide detection probe has a length of up to 18 nucleotides.

23. The composition of Claim 22, wherein the sequence of said oligonucleotide detection probe is selected from the group consisting of SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26 and SEQ ID NO:27.

24. The composition of Claim 23, wherein the sequence of the first amplification oligonucleotide is selected from the group consisting of SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18 and SEQ ID NO:19, wherein the sequence of the second amplification oligonucleotide is selected from the group consisting of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 and SEQ ID NO:7, and wherein the sequence of the oligonucleotide detection probe is selected from the group consisting of SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26 and SEQ ID NO:27.

25. A method for determining whether a biological sample comprising nucleic acids includes an HIV-2 nucleotide base sequence, said method comprising the steps of:

contacting the nucleic acids of the biological sample with a composition comprising,

a first amplification oligonucleotide comprising a sequence of 9-34 contiguous bases contained within the sequence of SEQ ID NO:9, said first amplification oligonucleotide having a length of up to 100 nucleotides, and

a second amplification oligonucleotide comprising a sequence of 19-40 contiguous bases from the sequence of SEQ ID NO:1, said second amplification oligonucleotide having a length of up to 100 nucleotides;

amplifying any of said HIV-2 nucleotide base sequence present in said biological sample to produce amplified nucleic acids; and

detecting said amplified nucleic acids produced in the amplifying step, whereby detection of said amplified nucleic acids indicates that said biological sample included the HIV-2 nucleotide base sequence.

26. The method of Claim 25, wherein the length of the first amplification oligonucleotide is 18-60 nucleotides, and wherein the length of the second amplification oligonucleotide is 19-40 nucleotides.

27. The method of Claim 26, wherein said first amplification oligonucleotide is a promoter-primer, and wherein the amplifying step comprises amplifying by TMA.

28. The method of Claim 26, wherein the detecting step comprises first hybridizing the amplified nucleic acids with a hybridization assay probe specific for said amplified nucleic acids, and thereafter measuring an amount of said hybridization assay probe that hybridized said

amplified nucleic acids.

29. The method of Claim 28, wherein the hybridization assay probe is a labeled nucleic acid probe.

30. The method of Claim 28, wherein the hybridization assay probe comprises the sequence of SEQ ID NO:21 or the complement thereof, said hybridization assay probe having a length of up to 22 nucleotides.

31. An oligonucleotide comprising the sequence of SEQ ID NO:21 or the complement thereof and a detectable label, said oligonucleotide having a length of up to 35 nucleotides.

32. The oligonucleotide of Claim 31, wherein the length of said oligonucleotide is up to 22 nucleotides.

33. The oligonucleotide of Claim 32, having at least 16 contiguous nucleotides contained within the sequence of SEQ ID NO:20 or the complement thereof.

34. The oligonucleotide of Claim 33, wherein said oligonucleotide has the sequence of SEQ ID NO:20 or the complement thereof.

35. The oligonucleotide of Claim 33, wherein said oligonucleotide has a length of up to 18 nucleotides.

36. The oligonucleotide of Claim 35, wherein the length of said oligonucleotide is 18 nucleotides.

37. The oligonucleotide of Claim 35, wherein said oligonucleotide has a sequence selected from the group consisting of SEQ ID NO:22 or the complement thereof, SEQ ID NO:23 or the complement thereof, SEQ ID NO:24 or the complement thereof, SEQ ID NO:25 or the complement thereof, SEQ ID NO:26 or the complement thereof, and SEQ ID NO:27 or the complement thereof.

38. The oligonucleotide of Claim 31, wherein said oligonucleotide comprises DNA.

39. The oligonucleotide of Claim 31, wherein said oligonucleotide comprises at least one nucleotide analog.

40. The oligonucleotide of Claim 39, wherein said at least one nucleotide analog comprises a methoxy group at the 2' position of a ribose moiety.

41. The oligonucleotide of Claim 37, wherein the detectable label is a chemiluminescent label or a radiolabel.

42. The oligonucleotide of Claim 41, wherein the detectable label is an acridinium

ester.

43. A method for detecting the presence of HIV-2 nucleic acids in a biological sample, comprising the steps of:

(a) providing to said biological sample a hybridization probe comprising the sequence of SEQ ID NO:21 or the complement thereof and a detectable label, said oligonucleotide having a length of up to 35 nucleotides;

(b) hybridizing under a high stringency condition any HIV-2 nucleic acid that may be present in the biological sample with said hybridization probe to form a probe:target duplex; and

(c) detecting said probe:target duplex as an indicator of the presence of HIV-2 in the biological sample.

44. The method of Claim 43, wherein the length of the hybridization probe in the providing step is up to 22 nucleotides.

45. The method of Claim 44, wherein said biological sample is a blood product selected from the group consisting of plasma and serum.

46. The method of Claim 45, wherein before step (a) there is a step for releasing nucleic acid from any HIV-2 that may be present in said biological sample.

47. The method of Claim 46, further comprising a step for capturing onto a solid support the nucleic acid released from said any HIV-2 that may be present in said biological sample.

48. The method of Claim 44, wherein said biological sample is a lysate.

49. The method of Claim 44, wherein said high stringency hybridization condition comprises 0.48 M sodium phosphate buffer, 0.1% sodium dodecyl sulfate, and 1 mM each of EDTA and EGTA.

50. The method of Claim 44, wherein said high stringency hybridization condition comprises a salt concentration in the range of 0.6 - 0.9 M.

51. The method of Claim 44, wherein the hybridization probe in step (a) has a sequence selected from the group consisting of SEQ ID NO:22 or the complement thereof, SEQ ID NO:23 or the complement thereof, SEQ ID NO:24 or the complement thereof, SEQ ID NO:25 or the complement thereof, SEQ ID NO:26 or the complement thereof, and SEQ ID NO:27 or the complement thereof.

52. The method of Claim 51, wherein the hybridization probe comprises at least one

nucleotide analog.

53. The method of Claim 51, wherein the hybridization probe comprises a detectable label.

54. The method of Claim 53, wherein the detectable label is an acridinium ester, and wherein the detecting step comprises performing luminometry to detect any of said probe:target duplex.

55. A kit for detecting HIV-2 nucleic acids, comprising:

(a) a first amplification oligonucleotide comprising a sequence of 9-34 contiguous bases contained within the sequence of SEQ ID NO:9, said first amplification oligonucleotide having a length of up to 100 nucleotides; and

(b) a second amplification oligonucleotide comprising a sequence of 19-40 contiguous bases from the sequence of SEQ ID NO:1, said second amplification oligonucleotide having a length of up to 100 nucleotides.

56. The kit of Claim 55, further comprising:

(c) an oligonucleotide detection probe that comprises the sequence of SEQ ID NO:21 or the complement thereof, and a detectable label.